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Database :
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Maximum Match 1008
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

BTU15731 25688 bp DNA linear MAM 04-SEP-2001 Bos taurus somalotropin receptor gene, exon 1 and liver-specific U15731 U15731 G1:13570031 Bos taurus Bos taurus Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora, Bovoidea;
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   242 CTAGGTCATCCGTCTTQCTGCAGATGACATTATTTCATTCTTTTAATGGCCGAGTAATA 301
                                                                                                                                                                                                                                                                                                                                                     62 ACCCTAACTATCTCCCCCCAGCTFTCCCCCCAGCAACCATAAACTCATTCTCTAAATC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                      2 TCGAGGATCCTTGTTCGTGTCCATTTTAAATATAGAAGTGTGTTCATGTCCATGCCCAAA 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    on Apr 10, 2001 this sequence version replaced gr. 560024.
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                                                                                                                                          1262 TATTITOAGALGILIGGALLGGGALLGLGGGAAATGTTGGGAGGGTGCGGTGTGGGAGAGA 1321
                                                                                                                                                                                                 8730 CCAGCCCCAAGCATICCAGCATICATICATICGAACCTIGGACTIGGCAACTICGTTGCTIACATIGA 8789
                                                                                                                                                                                                                                                          8490 ATAGCCACTGATAGGTACTATAATTAAACATGGAACTTTAAGTATGTTGGGATCTCCAAT 8549
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                                                                                                                     TO TOGO ATTICTICACIOTETICACO TEGO AATAGET LOCTET GATOTOCACAGO
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CAGCCCCTCTGGCGTATGGTCTTTGTCAAATTCTAATACGTGGCCTTCTCAGTTGGTCTG
                                                                                              GAGCTICCLICANCICCTIAGCIGIGGGALIAGATICCGACAACICTCCCIGTCIT 9929
                                                                                                                                                                                               CTUGCTATACTCTGGGGTTCTTGGGATCCTTCATGGAGATTCCAGCACCTCTGCCCTCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               picces.
AC119060
AC11906C.1
                                                                                                                                                                                                                                                                                                                         Submitted (24-APR-2002) NIH Intramural Sequencing Center, 8717 Spokement Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bos taurus clone RP42:30911, WORKING DEAFT SEQUENCE, 4 unordered
                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                  Green, K.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bovidae; Bovinae; Bos.
1 (bases 1 to 174419)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HTG: HTGS_PHASE1: HTGS_DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 174419)
                    Seguencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Biq Dye; 100% of rea
                                                                                                     Center project name: 30 Center clone name: 30
                                                                                                                                                                                      wcb sitc: http://www.nisc.nih.gov
Contact: nisc_zoo@nhgri.nih.gov
                                                                                                                                                                                                                                             Center: NiH Intramural Sequencing Center code: NISC
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program: Phrap; version 0.990319
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Db 120837 TATACATCAGIGICITTTIGCIGICICGIACACACACACHIALIGGIAICATCITCTAAA 120890
                                                                                                                                             Db 120717 GCATCATGCATCGAACCTGGACTGGCAACTCGTTTCCCACATGATACTTTACATGTTTCA 120776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 120537 TTTT111111116CCCIAALLITALEHTALEHTAACTTIACATAATTGTALTAGTTTIG 120596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Lival Similarly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                   120597 CCAAATATCAAAATGAATCCGCCACAGGTATACATGTGTTCCCCATCCCGAACCCTCCTC 120656
                                                                                       1338 TATACATGAGTGTCTCTTTTGCTGTCTCGTACAGGGGTTATTGTTAGCATCTTTCTAAA 1397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1398 FOCCATATATATOCOTTAGTATACTGTATTTATCTTTTTCCTTCTCCGCTTACTTTCACTCT 1457
                                                                                                                                                                 1.278 TEGCOATTCTCCCAAATCTTCCCACCCTCTCCCTCTCCCACAGAGTCCATAAGACTGTTC 1337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   arbittary.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working drait' sequence. It currently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Insert size: 14600; agarose-Ip
Insert size: 174119; sum-of-contigs
Insert size: 174119; sum-of-contigs
onality coverage: 10:13x in 020 bases, agarose fp
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Quality coverage: 8.50x in Q20 bases; sum-of-contigs
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clone_end:SP6
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/db_xre1-"taxon:9913"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39.3%; Score 1128.6;
94.4%; Pred. No. 2.4e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51204: contiq of 43679 bp in length 51303: gap of unknown length
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Db 121437 FOARGTGTGTTAGFCAGCCATCTGTAAGTCTGTTTTGGAGAAAGGTGTGTTTAGTTTGGTTTGG 121496
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                                                                        ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2117 GCTGTCTTTTCACCTTIGCTAATAGTTTCCTTTIGATGTTGCAGAAGCTTTTAAGGTTTAATTA 2176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1878
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                        HTG: HTGS_PHASE1; HTGS_DRAFT
                                                  AC119051.1 G1:20279432
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                                                                                                                              Bos taurus clone RP42-521B3, WORKING DRAFT SEQUENCE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bos taurus
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia, Pecora, Bovoidoa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 be preserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 208327)
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Insert size: 207827; sum-of-contigs
Quality coverage: 9-95x in Q20 bases, agarose fp
Quality coverage: 7.90x in Q20 bases, sum of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chemistry: Dye-terminator Hig Dye: 100% of reads Assembly program: Phrap: version 0.990319
Consensus quality: 206681 bases at least 040
Consensus quality: 207342 bases at least 020
Consensus quality: 207342 bases at least 020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing vector: plasmid: n/a: 100% of reads
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center project name: ddw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: nisc_zoo@nhgri.nih.gov
                                                                                                                                                                                                                                                                                                                                            56608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www.nisc.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center. WIH intramural sequencing Center Center code: NISC
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1. .6978
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156507: contig of 47463 bp in
156607: gar it takenwe length
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55366: gap of unknown length
108944: contig of 53578 bp in length
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7078: gap of unknown length
17342: contig of 10264 bp in length
17442: gap of unknown lenath
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Bust Local Similarity 94.4%;
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                 26918 TTTTTTTTTTCCCCTAATTTTATTTTATTTTTAAACTTTACATAATTGTATTAGTTTIG 26977
                                                                                                                                  27638 GTGGCTGTACTAGTTTGCATTCCCACCAACA64GAAGAGGGTTCCCTTTLCCCACACC
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                                                                                                                                                   Submitted (20 JUL 2002) NIB Intramaral Sequencing Center, 8717 Grovement Circle, Gaithersburg, MD 20877, USA on Jul 20, 2002 this sequence persion replaced 41.18581928.
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Center: NIH Intramural Sequencing Center
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Web site: http://www.nisc.nih.gov
Contact: nisc_zoo@nhgri.nih.gov
  Center clone name:
                   Center project name: cjq
                                        --- Project Information
399H12
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data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by 30k testing. In addition, the sequence assembly is based on at least 8% average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence are transfer by the sequence of the coverage of the sequence of the coverage of the sequence of the coverage of the sequence The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indivated order and orientation of each sequence config has been order and orientation of each sequence. with a Phrap-derived quality score. costigs have been trimmed away, and each base is associated established using one or more of the following: read pair

Insert size: 183000; agarose fp Insert size: 183804; sum of contings Quality eccerage: 12.04x in 920 bases; agarose ip Quality coverage: 10.68x in 920 bases, sum-of-contings Chemistry. Die terminaler Bia Tye: 100% of reads Assembly program: Phrap: version 0.990819 Consensus quality: 14972b bases at least 040 Consensus quality: 149872 bases at least 040 Consensus quality: 149872 bases at least 020 Sequencing vector: plasmid; n/a; 100% of reads

NOTE: This is a 'working draft' sequence, it currently consists of 2 contigs. Gaps between the contigs.
are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have * provided by the submittor.

This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

1 71025; contiq of /1025 bp in length 71026 71125: gap of upknown length 71126 149984: contig of 78859 bp in length Location/Qualifiers

PEATURES misc_feature /organism-"Bos laurus" /db_are1-"taxon:9913" /clone-"RP42-399H12" /clone_lib-"RP42" /note-"assembly_fragment

clone_end:SP6

vector_side:left"

misc_teature 71126 ...149984 /wote-"assembly_tragment clone_end:T7 /note: "clone overlaps with GenBank Accession Number AC109791 clone RP42-43317 (center project name cjf)" 1. .69714

BASE CHUNI ture 96712. 149984
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ORIGIN

Db 60956 CTCAATGTTGAGGTTTTTTTTTTTTTTTTTAATTTTTATTTTTAAACTTTAAACTTTACATAAT 61015 Query Match 38.8%; Score 1112.8; DH 2; Length 149984; Hest Local Similarity 93.0%; Pred. No. 1.5e-257; Matches 1198, Conservative 0. Mismatches 87; Indels 4; G 1627 STANTSTITIANATTITITITITITITIC LICENAL HILLING HILLIH 1; Gaps

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                                                                                                                                                                                                                              Submitted (20-JUL-2002) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA on Jul 20, 2002 this sequence version replaced gi:18581930.
                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (07-FEB-2002) NIH Intramural Sequencing Center,
Grovement Circle, Gaithersburg, MD 20877, USA
3 (bases 1 to 155794)
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HTG: HTGS_PHASE2: HTGS_DRAFT
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                           Center project Information
                                                                             Contact: nisc_zoo@nhgri.nih.gov
                                                                                                                                           Center: NIH Intramural Sequencing Center code: NISC
Center clone name: 433107
                                                                                                            Web site. http://www.nisc.nih.gov
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data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, its beind order and orderation of each sequence condig has been established using one or more of the following: read-pair the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out with a Phrap-derived quality score. contigs have been trimmed away, and each base gross misassemblies, the low-quality ends of sequence human), and/or confirmation by PCK testing. Sequencing vector: plasmid; n/a; 100% of reads In addition,

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Query Match
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* are represented as reasonal N. The ribs of the sizes
* is believed to be correct as given, however the sizes
* of the gaps between them are based an estimates that have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          thy the finished sequence as soon as it is available and the accession number will be preserved.

1 4357; contid of 4357 bp in length
43588 43657; gap of unknown length
43688 61202; contid of 17545 bp in length
61203 61302; gap of unknown length
61303 155794; contid of 94492 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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Insert size: 155594, sum of contlas
Onality coverage: 12.75x in G20 bases, agarose-fp
Quality coverage: 10.28x in G20 bases, sum of contlas
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Note: "Clear overlaps with General Arrecales Number Ar109789 clone 8042-99812 (center project name ejg)" a 28034 c 30648 g 50287 t 200 others
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clone_end:SP6
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/db.xrcf-"taxon:9913"
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        G6TCCCATTIGETTALTITIGETTTAETTCCAATATTCTGGGAGGTCGCGGAGATCGGGTCTCCCAGAA
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        CCTCCCATTIGETTATTTTTGATTTTAETTCCAATATTCTGGGCGCGCGCGCGCGCCCAFACACCACA
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DB 147830 CICICCATCATTCATTCATTGIAGACTTTGGAGCCAGCCAGCCAGCCAGCGGGGGGAAAT 147889
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                                                                                                                                                                                                                                      Submitted (25 JUL-2002) NIH Intramural Sequencing Center, 8717 Grovement Circle, Gaithersburg, MD 20877, USA On Jul 25, 2002 this sequence version replaced gi:18581929.
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Submitted (07 FEB 2002) NTH Intramural Sequencing Center, 8717
Grovement Circle, Caithersburg, MD 20877, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazca; Chordata; Craniata; Vertebrata; Euteleostemi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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Center clone name: 040N24
                                   Center project name: axl
                                                                                      Web site: http://www.nisc.nih.gov
Contact: nisc_zoo@nhgri.nih.gov
                                                                                                                                                         Center: NIH Intramural Sequencing Center Center code: NISC
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                                                         -- Project Information
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The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least BX average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

Sequencing vector plasmid, L/a, 100% of reads Chemistry, Dye terminator Hig Dye, 100% of reads Assembly program: Phrap, version 0.990319 (Consensus quality: 187613 bases at least Q40 (Consensus quality: 18781 bases at least Q20 (Consensus quality: 188010 bases at least Q20 (Consensus quality: 188010); sum-of-contigs Quality coverage: 9.14x in Q20 bases; sum-of-contigs

- * NOTE: This is a 'working draft' sequence. It currently consists of 5 contiys. Gups between the contiys are represented as runs of N. The order of the pieces are believed to be correct as given, however the sizes
- of the gaps between them are based on estimates that have
 provided by the submittor.
 This sequence will be replaced
- * by the finished sequence as soon as it is available and

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                                                                           Bos taurus
                                                                                                                              HIG: HIGS_PHASE2; HIGS_DRAFT.
                                                                                                                                                                                                                                                                                  Bos taurus clone RP42-87M16, WORKING DRAFT SEQUENCE,
Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Enteleostomi;
                                                                                                                                                                    AC109799.2 GI:21909466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Hansen, N., Ho, S.-L., Idol, J.R., Kardins, E., Larie, P., Lee-Lin, S., Q., Legaspi, R., Maduro, Q.L., Maduro, V.B., Marquiles, E. H., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Paguiriqan, C., Peatson, R., Portnoy, M.E., Prasad, A., Schueler, M.G., Stantripop, S., Thomas, J.W. Inomas, P.J., Touchman, J.W., Isurgeon, C., Voqt, J.L., Walker, M.A., Wetherby, K.D., Widqins, L., Younq, A., Zhang, L.-H. and Green, E.D., Nist, Comparative Sequencing Initialize
                                                                                                                                                                                                                                                                                          Submitted (19 JUL 2002) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (07-FEB-2002) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia, Eutheria, Cetartisdactyla; Ruminantia; Pecora; Bovoidea;
Bovidae, Bovinae, Bos.
                                                                                                                                                                                                                                                              on Jul 19, 2002 this sequence version replaced gl:18582079.
                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                               Green, E.D.
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wheter N | Antonollis A
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                                                                                          Web site: http://www.nisc.nih.gov
Contact: nisc_zoo@nhgri.nih.gov
Center clone name: 087M16
                        Center project name: axm
                                                                                                                                                                Center code: NISC
                                                                                                                                                                                            Center: NIB Intramural Sequencing Center
                                                           ---- Project Information
                                                                                                                                                                                                                                  Genome Center
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TITLE

COMMENT

3.17.13

Ine sequence data in this record represents an 'enhanced' version of a Phase 2 submission, Specifically, the indicated order and orientation of each sequence conting has been established using one or more of the following, lead-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., ${\rm human})_{\ell}$ and/or confirmation by PCR testing. In addition the sequence assembly is based on at least 8X average with a Phrap-derived quality score. centigs have been trimmed away, and each base is associated gross misassemblies, the low quality ends of sequence coverage in Q10 bases and has been reviewed to rule out In addition,

Insert size: 144000; agarose-tp Insert size: 187960, sum of contias Quality coverage: 18.54x in 020 bases; agarose-tp Quality coverage: 11.61x in 020 bases; sum of-contigs Summary Statistics
Sequencing vector: plasmid; n/a: 100% of reads
Chemistry: Sye terminator Big bye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 167942 bases at least 040
Consensus quality: 167948 bases at least 040
Consensus quality: 167968 bases at least 040

- are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes consists of 1 contigs. Gaps between the coulius NOTE. This is a 'working draft' sequence. It currently
- of the gaps between them are based on estimates that have
- provided by the submittor.
 This sequence will be replaced
- the accession number will be preserved. by the finished sequence as soon as it is available and
- /orqanism-"Bos taurus" /db_xref-"taxon:9913" Location/Qualifiers 167968 167968: contig of 167968 bp in length

FEATURES

source

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BASE COUNT
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Best Local
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AC109787
                                                                                                                                                Submitted (07-PEB-2002) NIH Intramural Sequencing Center, Grovement Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                    Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Prasad,A. Stantripop,S. Thomas, T.W., Thomas, P.J., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Ho, S.-L., Idol, J.R., Karlins, E., Larie, P., Lee-Lin, S.-Q., Legaspi, R., Maduro, Q.L., Maduro, V.B., Masielie, C., Maskeri, B.
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Bos taurus clone RP42-136015, WORKING DRAFT SEQUENCE.
                                                                                                                                                                                                                                  Green, E.D.
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                                                                                                                                                                                                         Direct Submission
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Mammalla, Eutheria, Cetartiodaetyla, Kuminantia, Pecora, Bovoidea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                   Unpublished
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                                                                                                                                                                                                                                                             (bases 1 to 154998)
                                                                                                                                                                                                                                                                                                            Comparative Sequencing Initiative
                           Contact: nisc_mouse@nhgri.nih
                                                                         Center: NIH Intramural Sequencing Center Center code: NISC
                                                 Web site: http://www.nisc.nih.gov
Project Information
                                                                                                                                Genome Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g,S.M., Benjamin,B.
Brinkley,C., Broc
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Db 120635 AATATCAAAATGAATCCACCCCAGGIATACATGTGTTCCCCCAGCCTGAAGCCTGCTCCCC 120694
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runs of N, but the exact sizes of the gaps are unknown
This record will be updated with the finished sequence
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Consensus quality: 154346 bases at least 040
Consensus quality: 154415 bases at least 030
Consensus quality: 154449 bases at least 020
Consensus quality: 154549 bases at least 020
Consensus quality: 154549 bases at least 020
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/clone="RP42-136015"
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154998: contig of 88595 bp in length
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                                                                                                                                   2180 CCCATTTGTTTAITTTTGCTTTTATTTTCCAATATTCTCGCACCTC 2224
                                                                                                                                                                                                                                                                                                                                               2120 GICUVETCACCITIGCTAATAGTETCCTTTGATGTGCGCAGAGCTTTTAAGGTTAATTAGGT 2179
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ORGANISM Hos taurus HTG; HTGS_PHASE1; HTGS_DRAFT Bos taurus. AC119060.1 G1:20279429 AC119060 HOS TAUTUS CLONE RP42-30911, WORKING DRAFT SEQUENCE, 4 unbordered

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REFERENCE Akhter, N., Astosellis, A., Bovidae; Bovinae; Bos. 1 (bases 1 to 174419) Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Cetartiodactyla: Ruminantia: Pecura: Bovoidea Ayele, K., Beckstrom Sternberg, S.

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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           as soon as it is available and the accession number will
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Insert size: 174119; sum-of-contigs
Quality coverage: 10.13x in Q20 bases; agarose-fp
Quality coverage: 8.50x in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing vector: plasmid; n/a: 100% of reads
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7525
                                                                                                                /note="assembly_fragment"
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103443, .174419
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7524: qap of unknown length
51203: contig of 43679 bp in length
51303: gap of unknown length
103342: contig of 52039 bp in length
103442: gap of unknown length
174419: contig of 70977 bp in length
                                                                                                                                                                                                                                                                                                                                                           .103342
    Score 1089.2;
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NOTE: This is a 'working draft' sequence, it currently
consists of 4 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Caps between the contigs are represented as

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Akhter.N., Ayele K. Bookstrom-Stornborg, S.M., Benjamin, B., Blakesley, R.M., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Badhighl, P., Bo, S.-L., Idol, J.R., Karlins, E., Larle, P., Lee-Lin, S.-Q., Legaspi, R., Maduro, Q.L., Maduro, V.B., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskoy, J.C., McDowell, J., Pearson, R., Prasad, A., Mastrian, S.D., McCloskoy, J.C., McDowell, J., Pearson, R., Prasad, A., Stantripop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Tsurqeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhaug, L. H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (08:FEB-2002) NIH Intramural Sequencing Center, 8717 Grovement Circle, Gaithersburg MD 20877 MSA
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Hos faurus clone RP42 262019, WERKING DRAFT SEQUENCE, 4 unordered
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Mammalia: Eutheria: Cetartiodaetyla: Ruminantia: Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HTC: HTGS_PHASEL: HTGS_DRAFT
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                                                                                                                                                                                                                                                                                                                                                                                                                              Suppose the Summary Statistics Sequencing sector. Flamid. a.a. 100% of reads Chemistry: Dye-terminator Big Dye, 100% of reads Assembly program: Phrap: version 0.990319 Consensus quality: 1767% bases at least Q30 Consensus quality: 177014 bases at least Q30 Consensus quality Q50 Consensus quality Q50 Consensus quality Q50 Consensus q50 Consen
                                                                                                                                                                                                                                            Insert size: 146000; agaroso-fp
Insert size: 177228; sum-of-contids
Quality coverage: 12.80x in 220 bases, agarase 16
Quality coverage: 10.59x in Q20 bases, saw of-contids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conter clone name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project name: cbc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: nisc_mouse*nhqri.nih.qov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: NIH Intramural Sequencing Center Center code: NISC
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1583 CATCTAGGITGCITCCATGTCTGGCIAITATAAACAGTGCTGCGATGAACATTGGGGTA 1642
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6697
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Query Match 37.5%; Score 1077.2; DH 2; Length 178028; Best Local Similarity 92.4%, Fred. No. 5.7c 249; Matches 1166; Conservative 0; Mismatches 93; Indels 3; G
                                                                                                            73369 ATTCTCCCAAATCTTCCCACCCTCTCCCACAGAGTCCATAAGACTGTTCCATAC 73428
73609 GAGTAATACTGCAFTGTATATGTACCAAAGCFFFGTTATCCATTCATCTGCTGATGCA 73668
                                                                                                                                                                                                                            73489 HATATATGAGTTAGTATAGTGTTTTTTTCTTTGCTTACTTCACTCTGTATA 73548
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                                                                                                                                                                                                                                                                                                                                                                        1343 ATGAGTGTCTCTTTTGCTGTCTCGTAAAACGGGGTAATGGTAACAACTTLTCTAAAACCCA 1402
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                                                                                                                                                                   1463 ATAGGCTCCACTTCATCCACCTCATTAGAACTGATTCAAATGTALTCTTTTTTAATGCCT 1522
                                                                                                                                                                                                                                                                                      1403 TATATATGCGTTAGTATACTGTATTTATGTTTTTCCTTCTGGCTTACTTCACTCTGTATA 1462
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                                                   1523 GAGIAATIACTICCATTIGTGTATATGTACCACAGCTTTCTTATCCATTCATCTGCTGGTGATGGA 1582

    runs of N, but the exact sizes of the gaps are unknown
    This record will be updated with the finished sequence

    be preserved.

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32654 cap of unknown length
77060 contig of 44406 bp in length
77160 dap of unknown length
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                                                                                                                                                                                                                                                                                                                 Bos taurus
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                                                                                                                                                                                                                       Submitted (02-A03-2002) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA 66. Aug 2, 2002 this sequence version replaced gi:18464071.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Portnoy, M.E., Prasad, A., Schueler, M.G., Stantripop, S., Thomas, J.W., Thomas, F.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, H.D. NISC Comparative Sequencing Initiative
                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (01-FFH-2002) NIH Intramural Sequencing Center, Grovement Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                Green, E.D.
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                     Center project information
                                                                              Contact: nisc_zoo@nhgri.nih.gov
                                                                                                                                                                                                  ---- Genome Center
Center clone name: 088B14
                                                                                                             Web site: http://www.nisc.nih.gov
                                                                                                                                        Center: NIH Intramural sequencing Center Center
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The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the hid/cated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated h.man; and/or confirmation by MCR testing. In addition the sequence assembly is based on at least 8x average with a Phrap-derived quality score. coverage in 220 bases and has been reviewed to rule out clones, alignment with available reference sequence (e.g., In addition,

Summary Statistics
Sequencing vector: plasmid: n/a; 100% of reads
Chemistry. Dye terminator Big Dye, 100% of reads
Assembly program. Phrap: version 0.990319
Consensus quality: 189385 bases at least 040
Consensus quality: 189385 bases at least 030
Cheseus quality. 189365 bases at least 030
Cheseus quality. 189365 bases at least 030
Insert size: 189478, sum of contigs
Ouality coverage: 11.72x in 020 bases; agarose fp Quality coverage. 8.23% in Q20 bases, sum of contigs

- consists of 7 contigs. Caps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes NOTE: This is a 'working draft' sequence. It currently
- of the gaps between them are based on estimates that have
- provided by the submittor.
 This sequence will be replaced
- by the finished sequence as soon as it is available and
- the accession number will be preserved.

 7696: contig of 7696 bp in length
- FEATURES 31715 31815 35939 7697 7797 14652 14752 26767 26867 Location/Qualifiers 95329. gap of wiktown length 1900/8: contig of 94749 bp in length 14651: contiq of our 14751: gap of unknown length 26766: centig of 12015 bp in length 26866: gap of unknown length 31714: contig of 4848 bp in length 31814: gap of unknown length 35938: contig of 4124 bp in length 36038: gap of unknown length 95229: contig of 59191 bp in length 7796: gap of unknown length .4651: contig of 6855 bp in length

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                                                                                                                                                                                                               100895 CARCHGOTGATGGACARCTAGGFFGCFFCCAFGFCCTGGCTACTATAAACAGFGCFGCGA 100836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101195 CATOTETICAATIGCCAFFCTICCCAAATCFFCCCACCCTCTCCCCTCTCCCACACACTCCATA 101136
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                                                                                                                                                                                                                                                                                                                                                                                                                                     100955 TCAFFTTANTGOCTGAGAAAAAACACACTGGGTALAFGFAACAGCAGCTGCCTTATCCAFF 100890
                                                  1629 TGANGATTAGASTACACGTGTGTGTTTGGGTTGTGGTTGGGTAGTATGGCCAGA 1688
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JOURNAL
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Arkhter, M., Ayele, K., Beckstrom-Sternberg, S.M., Henjamin, H., Arkhter, M., Ayele, K., Beckstrom-Sternberg, S.M., Hrinkley, C., Brooks, S., Blakesley, R.M., Cupita, J., Hadhidhi, P., Dietrich, N.L., Granite, S., Chan, X., Gupta, J., Hadhidhi, P., Dietrich, N.L., Granite, S., Chan, X., Gupta, J., Hee-Lin, S., Q., Lequspi, R., Maduro, C.L., Maduro, V.B., Masiello, C., Maskeri, B., Masierian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Prasad, A., Stantripop, S., Thomas, J. W., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Vogt, M.A., Wiggins, L., Vogt, M.A., Wetherby, K.D., Wiggins, L., Vogt, M.A., Wetherby, K.D., Wiggins, L., Vogt, M.A., Wiggins, L., Vogt, M.A., Wetherby, K.D., Wiggins, L., Vogt, M.A., Wiggins, L., Vogt, M.A., Wiggins, L., Vogt, M., Vo
Direct Submission
                                               Green, E.D.
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Bos taurus clone RP42-505C3, WORKING DRAFT SEQUENCE, 4 unordered
                                                                                                                                         Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Cetartiodaetyla; Ruminantia; Pecora; Bovoidea
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                                                                                                                                                                                                                                                        Young, A., Zhang, L.-H. and Green, E.D.
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                                                                                                                                                                                                 63156 TTTTTTTTTTTTAAACTTTACATAATTGTATTAGTTTTGCCAAATATCAAAATGAAT 63097
63036 CATCCCHORGGETOGRECOCAGTGCACTAGCCCCAAGCATCCAGTARCATGCATCGAACCT 62977
                                                                                                  1058 TITTATTTTATATTTAAACTTTACATAATTGTATTAGTTTTGCCAAATATCAAAATGAAT 1117
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                                             1178 CATCCCTCTGGGCCG-CCCAGTGCTCCAGCCAGCCATCCAGCATCATGCATGGAACCT 1236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
                                                                                                                          Submitted (97 FEB 2002) NIH Intramural Sequencing Center, 8717 Grovement Circle, Gaithersburg, MD 20877, USA
                          consists of 4 contigs, the true order of the pieces is not known and their order in this sequence record is arbitrary. Saps hetween the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                   86009
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Insert size: 204840; sum-of-contigs
Quality coverage: 13.17x in 020 bases; agarose fp
Quality coverage: 9.52x in 020 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: NIH Intramural Sequencing Center Center code: NISC
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4719
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/clone="RP42-505C3"
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4718: gap of unknown length
11439: contig of 6721 bp in length
11539: gap of unknown length length
100659: contig of 89120 bp in length
100759: gap of unknown length
205140: contig of 104381 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (29-NOV-2001) Department of Biology, Center for Biomedical Research, University of Victoria, PO Box 3020 STN CSC, Victoria, British Columbia VBN 3N5, Canada
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Mammalia; Eutheria; Cetartlodactyla; Ruminantia; Pecora; Bovoidea
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/gene="TCRBJ1"
                                                                     /qene-"TCRBJ2"
                                                                                                                                                                                            /note-"RSS nonamer"
                                                                                                                                                                                                                                              /note-"RSS spacer"
                                                                                                                                                                                                                                                                                                                    /gene-"TCRBD1"
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1094 GTTTTGCCAAATATCAAATCAATCCGCCACAGCTATACATGTGTTCCCCCATCCGGAACC 1153	1034 TITAAATTTITTTTTTTTTTCAATIITATTITATTTTTAAACTTTACATAATTGTATTA 1093 	Query Match 37.3%; Score 1069; DB 4; Length 151482; Hest Local Similarity 91.2%; Prod. No. 5.4e-247; Matches 1168; Conservative 0; Mismatches 110; Indels 3; Gaps 3;	/gene."TCRB36" /note-"TCR beta J6 segment" 32430. 34057 /gene-"TCRBC3"	mlsc_signal 28646. 28652 /qene-"TCRBJ6" /note="RSS heptamer" J_segment 28653. 28699	/note="RSS nonamer" 286.4428645 /gene="TCRBJ6" /note="RSS spacer"	genc 2862528639 /gene="TCRBJ6" misc_signal 2862528633 /gene="TCRBJ6"	/note="RSS heptamer" J_segment 2858: .28415 /aene-"TCRB55" /note-"TCR beta J5 segment"	/gene-"TCRBJ5" /note="%SS spacer" misc_signal 28361. 28367 /gene-"TCRBJ5"	misc_signal 2834028348 /gene_*ICRHJ5" /note="RSS nonamer" misc_signal 2834928360	/uene-"TCRBH4" /note-"TCR beta J4 segment" /sene 28410. 28415 /gene-"TCRBJ5"	misc_signal 2824328249 /gene="TCRB44" /note="KSS heptamet" J_segment 2825028298	/note-"RSS nonamer" 28241, .28242 /webe-"TNR54" /note-"RSS spacer"	gene 2822228298 /qene="TCRBJ4" misc_signal 2822228230 /qene="TCRBJ4"	gment	/gene-"NCRBJ3" /note-"RSS spacer" misc_signal 28026. 28032 /gene-"TCRBJ3"	misc_signal _20005200]	/note=""CR beta J2 segment" gene 2800528083 /gene=""CRBJ3"
3311 TAATTAGGTCCCATTGTTTATTTTGCTTTATTTCCAATATT:TGGGAGGTGGGTCAT	OY 211 CHARASSI HICH HILL CHARLES HAVE HICH HIGH SIN-MARKETH HARGET 2170	2051 IGTATATTITTAGATATTAGTOGRIFACTOATITGCIAHIAHIHIKOTOCATT	Oy 1991 CT Db 3491 CT	Qy 1931 ATCTITICATGTGTITGTTAGCCATCTGTATGTCTTTTTGGAGAAAATGTCTATITAGTT 1990 	QY 1872 TGAAATGGTACCTCATAGTGG-TTTGATTTGCATTTCTCTGATAATGAGTGAGGTTGAGC 1930	Gy 1812 CACACCCICICCAGCAILLALLALLIGITGIAGACHILIGGAICCGACCAALCTGACTGCTG 1871 	QY 1752 TCCATAGTGGCTGTACTAGTTTGCATTCCCACCACAGTGTAAGAGGGTTCCCTTTTCTC 1811	Qy 1692 GGGTTGCTGGATCATAAGGCAGTTCTATTTCCAGTTTTTTAAGGAATCTCCACACTGTTC 1751	Qy 1632 ACATIGAGAI ACAGAGACICICT FICCOLLEGGI FFCCTCAGTGIGIAIGCCCAGCAGTG 1691 	UY 1572 (TSATGANGAPATAGGIPA) HANAGGANGANTATATATAAA AWITATGAGATGA 1631 	Qy 1512 TITTAATGGCTGAGTAATACTCCATTGTGTATATGTACCACAGATTTCCTTATCCATTCAT 1571 	Oy 1452 CACTOTGFAFAATAGGCTCCAGTTTCATCCACCTCAGTTAGAACTGATTCAAAGGFATTCT 1511 	0) 1392 TCTANATCCCATATATATGCGTTAGTGTATITATGTTTTTCCTTCTGGCTIACTT 1451 	1332 C	QY 1272 GTTTCATTGCCAAAGCTTCCCAAAGCCTCCCCCCCCCCACAAGCCCA4AAGA 1331 Eb 4211 STTTCAATSCCATTCCCCAAAGCTTCCCAACCCTCTCCCACAGAGTCCA4AAGA 1331 Eb 4211 STTTCAATSCCATTCTCCCAAAGCTTCCCAACCCTCTCCCACAGGTCCATAAGA 4152	1213 CADCASCATO 4271 CADCCAGTATE	$\alpha -$

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                                                                                                                                                                                                                                                                                                                                                                diternate chemistry, an assented by high quality data (i.e., phred quality > 40); an attempt was made to resolve all regions were covered by at least one plasmid subclone or more than one MI3 subclone; and the assembly was confirmed
                                                                                                                                                                                                                                                   CIONE LENGTH: This sequence represents the entire insert of
this close unless otherwise noted. If there are overlapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          enthitted (05 cm 2001) ARH Intramural Sequencing Center, 8717
Grovemont Circle, Caithersburg, MD 20877, USA
on Oct 6, 2001 this sequence version replaced gill4192894.
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Mammalia; Butheria; Cetartiodaetyla; kominantia; Pepera, Bovoidea,
Boridae; Dovinae; Pes
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                                                                                                                                                                                                                           clones, the overlaps are noted in the beginning and end of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             all regions were double-stranded, sequenced with an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (11-APR 2001) NIH Intramural Sequencing Center, 8717 Grovement Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tsurgeon, C., Yout, J.E., Walker, M.A., Wetherby, K.D., Wiggins, L., Zhang, L., H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        this sequence was finished as follows unless otherwise noted:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www.nisc.nih.gov
Contact: nisc_monscanhgri.nih.gov
--- Project Information
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center project name:
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                                                                                                                                                                                                   vatures section
                                                      /\db_arel="taxon.9913"
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Best Local Similarity 91.3
Matches 1160: Conservative
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                                                                                                                                                                                                                                                                                                                                  100458 CATCTAGGTFIGGTFIGGATG FCCTGGGCTATTAGAAAAGAGTGCTGGGGATGAAGATTIGGGGTG 100517
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                                                 1763 FOTACTAGTITGCATTOCCATTOCAGCAACAGTGTAAGAGGGTTOCGT FF FCFOCAGAGAGGGTCTC
                                                                                                                                                                                                                                    1703 TCATAAGGCAGTTCTATTTCCAGTTTTTTTAAGGAATCTCCAGACTGTTCTTCATACTGCC 1762
                                                                                                                                                                                                                                                                                                                                                                                                                                4645 CANDONICIINOCHICIAGHIOCHOAGIGIAIAIG COAG AGGGGGITGCIGGA 1702
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            105167. .105288
/hote "single clone coverage"
135741. .135747
/hote "single clone coverage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Photo-"this sequence is not the entire insert of clone RM2-524024; clone everlups with GenBunk Accession Humber Accessive Incientides 148950 [62859] clone RM2-554K7 (center project name axw); this annotated seqment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-"single clone coverage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       160866.
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O. Mismatishes 107, Indels
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                                                                                                                                                         JOURNAL
                                                                                                                                                                                     TITLE
                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                         JOURNAL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100938 GAGATTAGITTGICAGITTGCTTCAFTIGCIAFTTTTTTTCTCCCCATTCTCAACCTTGT 150997
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                                                                                                                                                                                                                                                                                                                     Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Boutlard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Baqhiqhi, P., Ho, S.-L., Idol, J.R., Karlins, E., Laric, P., Lee-Lin, S.-O., Icgaspi, R., Maduro, O.L., Maduro, V.B., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Plasad, A., Stantripop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Voqt, J.L., Walker, M.A., Welherby, K.D., Wigjins, L., Young, A., Zhang, L.-H. and Green, E.D.
                                                                                                          Direct Submission
Submitted (07-FEB-2002) NIB Intramural Sequencing Center,
Grovemont Citcle, Gaithersburg, MD 20877. USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACTIO9794 166277 bp DNA linear I
                                                                                                                                                                                                                                                                                                  NISC Comparative Sequencing Initiative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryola; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC109794.1 GT:18582004
                                                                                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bovidae; Bovinae; Bos.
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                                                                                                                                                                                                                                             (bases 1 to 166277)
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                                  Center: NiH intramural Sequencing Center
Center code: NISC
Web site. http://www.nisc.nih.gov
                                                                                             Genome Center
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                                                                                                                                                                                                                                                                                         96394 CACCACAGGIATACCIGITTECCCATCCIGAACCCTCCCCCCCCCCCCCCCCCCCCCAIACC 9645.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96334 TITATTTTATATTTTAAACTTTACAATATTTTÄTTAGTTTTTGCCAGATATGGAAATGAATT 96393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96274 TCAGGTTGATAGGGGATGTAAAAGGAAGCAAATAACATTTTTTTAAAATITLITITIAAAT 96333
                                                        96574 CCCCACCCTCTCTCTCCCAAAGAGICCGTAAGACTGATTTATACATCAGGGICTCTTT 96633
                                                                                                                                                                              96514 GACIGGCGGCICGTIICAIACAIGAIAIIIIACAIGIIICAAIG CAIICICCCAAAICI 96573
                                                                                    1297 FOOTAGOCI CI GOCTAGAGAGAGI COATAAGACHG PECLAHAGARGAGI GICI CITIT 1356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1119 CGCCACAGGTATACATGTGTTCCCCATCCCGAACCCTTCCTCCTCCTCCTCCCCATACC 1178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOUTED
   1357 IGCIGICICGIACACCGGGITATIGITACCATCIITCIAAATCCCATATATATGCGTTAG 1416
                                                                                                                                                                                                                                    1236 GACTGGCAACTCG-TTCCTACATGATATTTCACATGTTTCATTGCCATTCTCCCCAAATCT 1296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 36.9%, Local Similarity 89.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the fluished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: This is a 'working draft' sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 51716: contig of 51716 bp in length
51717 51816: gap of unknown length
51817 166277: contig of 114461 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       quality coverage: 10.92x in Q20 bases; sum of contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Insert size: 143000; agarose-1p
Insert size: 166177; sum-of contigs
Quality coverage: 12.69x in Q20 bases, agarose-1p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Consensus quality: 166045 bases at least Q40 Consensus quality: 166067 bases at least Q30 Consensus quality: 166073 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap: version 0.990319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center project name: cj)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vector_side:right*
51817. .166277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone_end:SP6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clone_end:T7
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/clone="RP42-49936"
/clone_]ib="RP42"
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1. .156277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism-"Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1059.2; DB 2; Length Pred. No. 1.2e 244; 0; Mismatches 133; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              n/a: 100% of reads
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Length 166277;

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97294 AFFFAFFFFFCCGGAGFFGAGCTGTAGGAGTFGCFFGAGATFAGFFFTGAGATFAGFFFFFF97353 2076 GEGGETGCTTCATTGSTATFATTTCTCCCATTCTGAAGGETGTCTTTTCACCTTGCT 2135 97054 TTCCCACCAACAGTGTAAGAGAGTTCCCTTTTCTCCACACCCTCTCCAGGATTTATTGCT 97113 96634 TROTROTCATANAMAGABOLIAH GILAH GILAH GILAH HILIH 97534 GOAGAGIGITITG CIAIGITCICCICIAGGAGITTIAIAGITICIGG 97581 96754 (ATCKATCKATTAGAACTGATTCAAATGTATTCTTTTTAATGGCTGAGTAATACTCCAT 96813 9/474 TOCTTTTATTTCCAATATTCTG66A06T666T6ATAGAGGATCCTGCTGCTGATGTATGTT 97539 97174 GATTTGGALLIGIGIGALAALGAGGAGGLGALGAGAAGGLILILIGATGTTTGTTAGCCAT 97233 97114 FOFAGAGTETTGGAFGGGAGCGAFFCTGAGTGGTGTGAAATGGTAGCTGGTGATAGTFFFFF 97173 96994 TATTTCCAGTT1111AAGGAAICICCACACIGIICICCAIAGIGGCIGIACTAGTTGCA 97053 96934 AAFTOTGAFFFCCTCAGTGTGTTATGCCCAGCAGTGGGAFFIGCTGGATCATAAGGCAGTTC 96993 96874 CCATGTCCTGG.LATTATAAA.AstusTusbaTigAACATTGGGGLAA.AcoTGTCTCTTC 96933 96814 CONGITATATOTAGGAGAGCTTICCITATCCATCTGATCTGCTGATGGGCATCTAGGTTGCTT 96873 96694 TATACIGIALLOGIGILLI ICLI ICIOGETIAGI ICACICIGIAIAAIAGGITECAGTTT 1896 GATHGCATITCTCIGATAATGAGGAGTGTGAGGAGTGTTTCATGTGTGTGTTAGCCAT 1955 | 1417 | FALACTIGTATICTEATICTECTICTICTICCTICACTICTICTATIANTAGE | ACCIONAL | A 1897 TGAWACTI I 166A FORCAGO AA FORGACTIGA CEGTGTGAAATGGTACCT CA I AGT - GGTTT - 1895 1777 PTOCOACCAACACTGTAAGAGGGTTCCCCPFFFCCTCCACACCCFCTCCCAGCAFFTTAFFTATT 1836 2737 FARHAN AGEETHIAANAAARCDAAAAGGTATIKAKAALAAJAGAAGAAGAAGIIIGGA 1776 1547 TGTGTATATGTAXXCACAGCTTTCTTATCCATTCATCTGCTGATGGACATCTAGGTTGCTT 1596 2256 FCACCCTTCATTTAACAAATATTCCACTTGCTATACTCTGGGTTCTTG 2303 2196 TGCTTTTATTTC.AA1A11C1GGAAGJIGGGTCTCCCAGAATGTTTTAAAATTTAATTGC 2255 1657 CCTTCTGGTT4CC1CA616F65A4682CA66CA616G6654G6CFGGA1CA5AA66CAG41C 1716 1597 COATGICCTCGCTATTATAAACAGTGCTGCGATGAACATTGGGGGTACACGTGTCTCTTTC 1656 1477 CATCCACCICALIAGAN/IGALICANALGIALICTELITANIGGCIGAGTNATACTCCNT 1536

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